FIG. 1

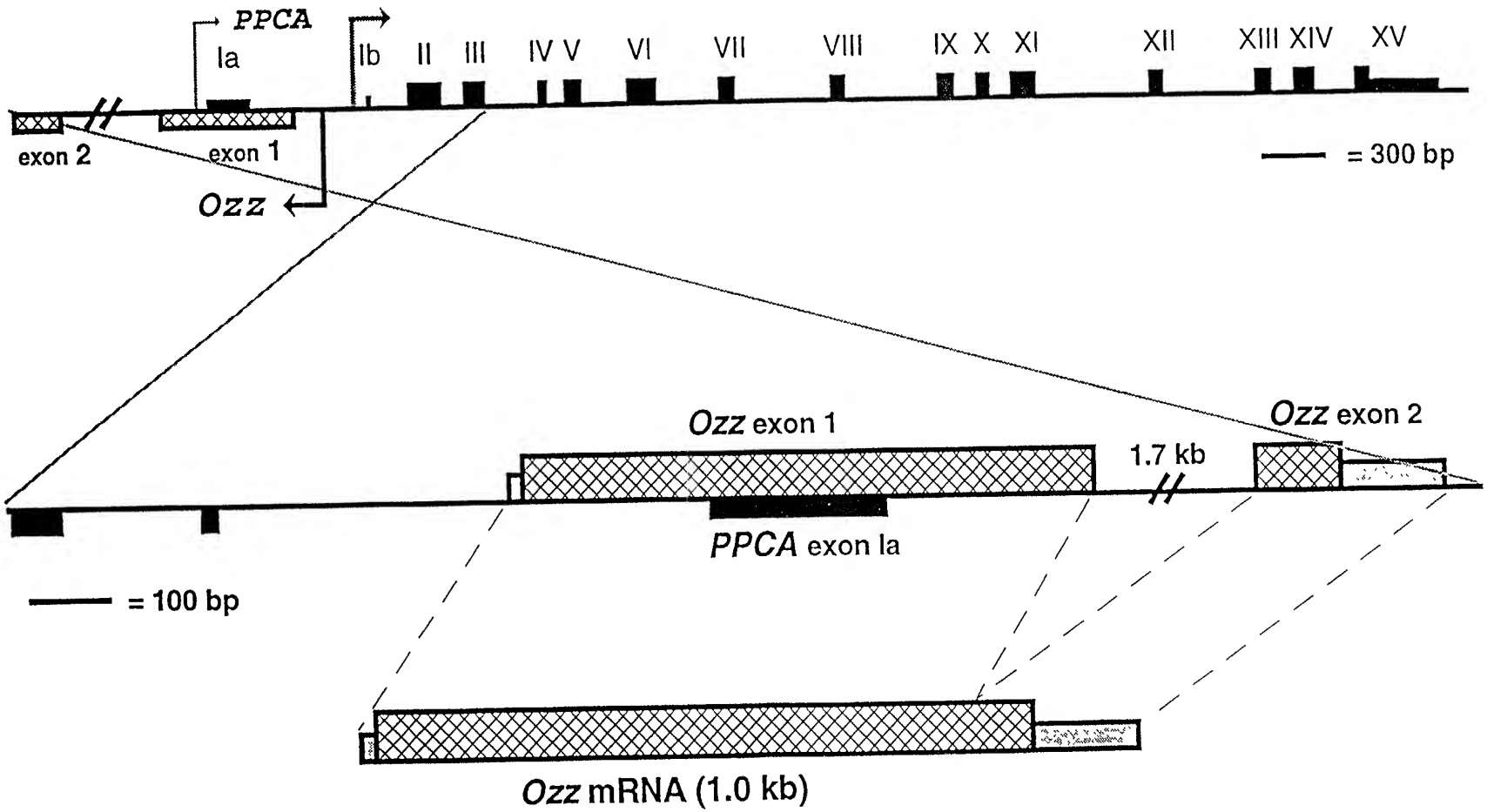

PPCA
Ia
Ib
II
III
IV V
VI
VII
VIII
IX X XI
XII
XIII XIV
XV
exon 2
exon 1
Ozz
= 300 bp
Ozz exon 1
Ozz exon 2
1.7 kb
PPCA exon Ia
= 100 bp
Ozz mRNA (1.0 kb)

FIG. 2A

```
   1  CCCTGTTGCA CGGCTTGGAG ATGGCTGCTC CCTCCGAACA CGTAGGACTG
  51  GGTGCCCCAC GGAGCCCTGC GCGCCCAGAG CCCCCTCCCA CCCGCTTCCA
 101  CCAAGTGCAT GGAGCCAACA TCCGCATGGA CCCCTCAGGA ACGCGAGCCA
 151  CACGCGTGGA GAGTTTCGCC CACGGTGTGT GCTTCAGTCG TGAGCCCCTG
 201  GCCCCCGGCC AGGTATTTCT AGTGGAAATT GAGGAAAAAG AGCTGGGCTG
 251  GTGCGGGCAC CTACGTCTTG GCCTGACCGC TCTGGATCCC GCCAGTCTGG
 301  CCGCTGTACC CGAGTTTTCA CTGCCTGACT TGGTCAGCCT TGGCCACAGT
 351  TGGGTCTTCG CTATCACACG CCACCACAAC CGTGTGCCCC GGGAAGGTCA
 401  ACCAGAAGCG GAGGCAGCGG TCCCCAGTGG TCCCCAAGCC CTACTGGTTG
 451  AACCCTATCT GCGCATCGAG CAGTTCCGAA TTCCCCGGGA CCGTCTGGTG
 501  GGCCGCAGCC GGCCAGGGCT TTATAGCCAC CTCTTAGATC AGCTCTATGA
 551  ACAAAACGTG CTGCCTCCTA CAGCGCGCCG AAGCCGCTTG GGTGTTCTCT
 601  TCTGCCCCCG TGAGGATGGG ACCGCCGACA TGCACATCAT CATCAACGGG
 651  GAGGACATGG GCCCTAGCGC CCGGGGGCTG CCAGCTGCTC AGCCCCTCTA
 701  CGCTGTGGTA GATGTGTTTG CTTCCACCAA GAGCGTGCGT CTGGTCCAGC
 751  TGGAGTATGG CTTGCCATCT CTGCAGACTC TGTGCCGACT AGTGATCCAG
 801  AAGAGGGTGG TACACAGGCT GGCCATTGAT GTGCTCCACC TGCCCAAAGG
 851  ACTGAAGGAC TTCTGCAAGT ACGAATGAAC GAATGAACGC CTGTCTGTGG
 901  CCACCAGAGC AAAGTCCCCG GTGGTGCGCC CTGCCTCTAG AGAAGTGGCT
 951  AGTCTGAAGC TGGTCGCACA GCTCACAATC AGGGCTGGAA ATAAATAGAG
1001  CCGATGTGGA TGTTCTGAGA AAAAAAAAAA AAAAAA
```

FIG. 2B

CCTGCCCTAT GGCCGAGAGA TGGCTGCTGC CTCCGAGCCC GTGGATTCGG GTGCACTCTG GGGACTCGAG

CGCCCGGAGC CCCCTCCCAC CCGCTTCCAT CGGGTGCACG GTGCCAACAT CCGCGTGGAC CCCTCTGGGA

CGCGGGCCAC ACGCGTGGAG AGCTTCGCCC ACGGCGTGTG CTTCAGCCGC GAGCCGCTGG CCCCGGGCCA

GGTCTTCCTG GTCGAGATCG AGGAGAAAGA GCTGGGCTGG TGCGGACATC TGCGTCTCGG TCTGACCGCG

CTGGACCCCG CCAGTCTGGC CCCCGTTCCC GAGTTTTCTC TGCCCGATCT GGTCAACCTG GGCCACACCT

GGGTCTTCGC CATCACGCGC CACCACAACC GCGTGCCCCG GGAGGGCCGC CCGGAGGCGG AGGCAGCGGC

CCCCAGCCGA CCTCCAACCC TCCTCGTGGA ACCATATCTG CGCATTGAGC AGTTTCGCAT TCCCCGGGAC

CGCCTGGTGG GCCGCAGCCG GCCAGGGCTC TACAGCCATC TCTTGGACCA GCTCTATGAG CTGAACGTGC

TGCCTCCGAC CGCGCGCCGT AGCCGCCTGG GTGTCCTCTT TTGCCCGCGC CCCGATGGCA CGGCCGACAT

GCACATCATC ATCAACGGCG AGGACATGGG CCCGAGCGCC CGGGGACTGC CAGCTGCGCA GCCCCTCTAC

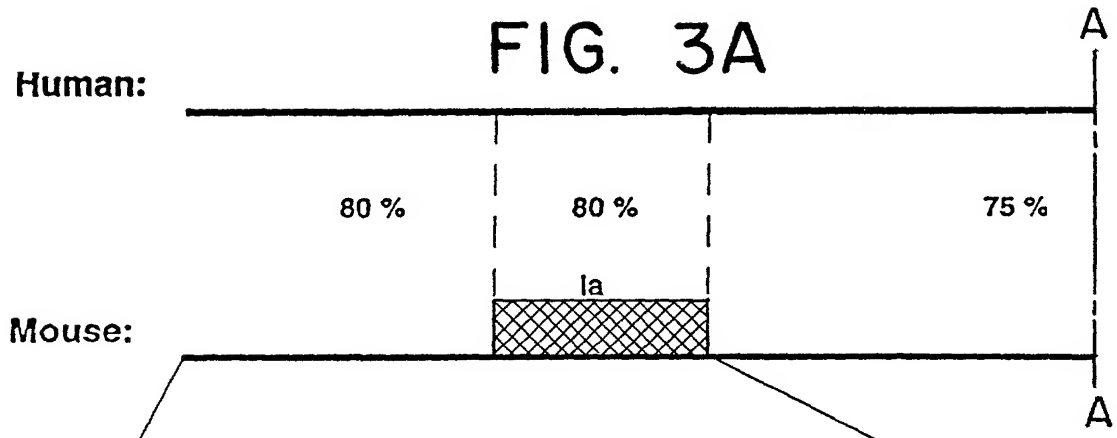
GCGGTGGTGG ACGTGTTTGC TTCCACAAAG AGCGTGCGCC TTGTCCAGCT CGAGTATGGC TTGCCATCCC

TGCAGACTCT GTGCCGCCTA GTGATACAAA GGAGCATGGT GCACCGGCTG GCCATTGATG GGCTCCACCT

GCCCAAAGAA CTTAAGGATT TCTGCAAGTA TGAGTGAAGA CCCACAGTGC ACCAGAGCAC AGCTGCATCC

TGGAGCCCCA GACCTGTGGC TGGCTGGTCC GAAGTTGGCC ACATTGCTGC CAGCCAAGAC

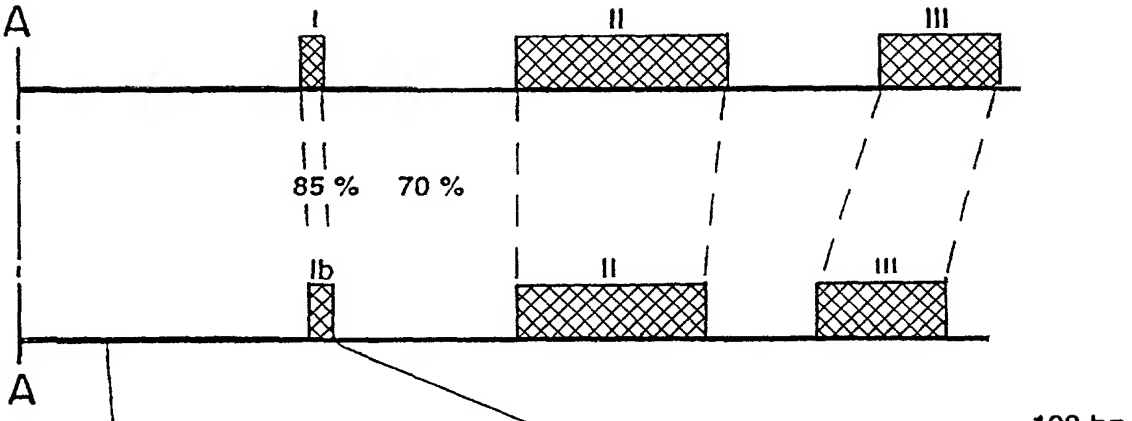
FIG. 3A



distal promoter

```
AGCCATACTCGAGCTGGACAAGGCG.CACGCTCTTTGTGGAAGCAAACAC
AGCCATACTCCAGCTGGACCAGACGCCACGCTCTTGGTGGAAGCAAACAC
                                        AP-2
GTCCACCACCGCGTAGAGGGGCTGCGCAGCTGGCAGTCCCCGGGCGCTCG
ATCTACCACAGCGTAGAGGGGCTGAGCAGCTGGCAGCCCCCGGGCGCTAG
          GRE
GGCCCATGTCCTCGCCGTTGATGATGATGTGCATGTCGGCCGTGCCATCG
GGCCCATGTCCTCCCCGTTGATGATGATGTGCATGTCGGCGGTCCCATCC
                    AP-2
GGGCGCGGGCAAAAGAGGACACCCAGGCGGCTACGGCGCGCGGTCGGAGG
TCACGGGGGCAGAAGAGAACACCCAAGCGGCTTCGGCGCGCTGTAGGAGG

CAGCACGTTCAGCTCATAGAGCTGGTCCAAGAGATGGCTGTAGAGCCCTG
CAGCACGTTTTGTTCATAGAGCTGATCTAAGAGGTGGCTATAAAGCCCTG
                                        TATA
..CCGCTGCGGCCCACCAGGCGGTCCCGGGGAATGCGAAACTGCTCAATG
GCCGGCTGCGGCCCACCAGACGGTCCCGGGGAATTCGGAACTGCTCGATG

CGCAGATATGGTTCCACGAGGAGGGTTGGAGGTCGGCTGGGGGCCGCTGC
CGCAGATAGGGTTCAACCAGTAGGGCTTGGGGACCACTGGGGACCGCTGC

CT..GCCTCCGGGCGGCC.TCCCGGGGCACGCGGTTGTGGTGGCGCGTGA
CTCCGCTTCTGGTTGACCTTCCCGGGGCACACGGTTGTGGTGGCGTGTGA

TGGCGAAGACCCAGGTGTGGCCCAGGTTGACCAAGATCGGGCAGAGAAAA
TAGCGAAGACCCAACTGTGGCCAAGGCTGACCAAG.TCAGGCAGTGAAAA

CTCGGGAACGGGGGCCAGACTGGCGGGGTCCAGCGCGGTCAGACCGAGAC
CTCGGGTACAGCGGCCAGACTGGCGGGATCCAGAGCGGTCAGGCCAAGAC
```

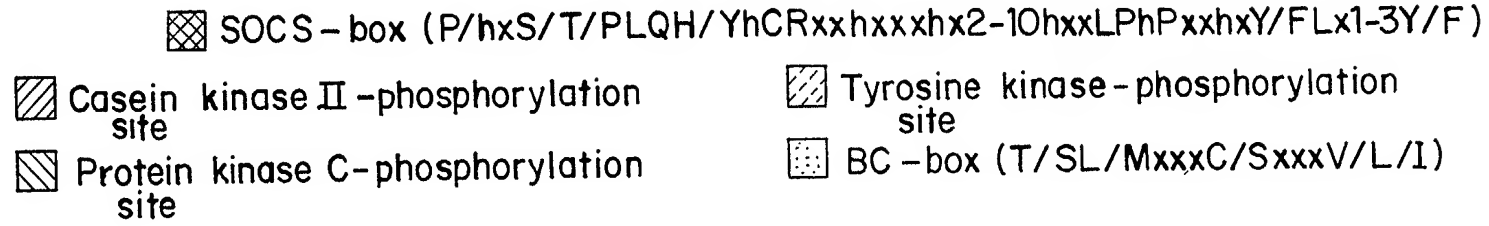
FIG. 3B



proximal promoter

```
                    .         .      Sp1      .         .         .
AGCTGGCGCCGGGGGCTATTTTGGGCGGCGGGCAATGATGGTGACCGCAA
||||   |||  ||||||||||||||| ||||||   |||  |||||
AGCTCATGCCAAGGGCTATTTTGGGCAGCGGGCTCAGATTGTGACGCGGG
                    .         .         .         .
GGCG.........ACCTTGTAAGGCATTTCCCCCCTGACTCCCTTCCCCG
||||          |||  ||||||||||||||||||  |   ||  |||||||
GGCGGGTGGATGAACCATGTAAGGCATTTCCCCCTTCTCTAACTTCCCCC
Sp1                 .         .         .      Sp1      .
AGCCTCTGCCCGGGGGTCCTAGCGCCGCTTTCTCAGCCATCCCGCCTA..
   |||||||  ||||||||||||||||||||||||      ||  |    ||
.AGCTCTGCCTGGGGGTCCTAGCGCCGCTTTCTCGCTTGTCACCAGTAAG
                    .         .         .         .
.....................CAACTTAGCCGTCCACAACAGGATCATCTGA
                        |||     | |||  |||  ||  |||||  ||||
GGGTCCCCAGGAGCCTGGGGAACCCTTCTGTCAACACCAAGATCACCTGA
                    .         .         .         .
TCGCGTGCGCCCGGGCTACGATCTGCGAGGCCCGCGGACCTTGACCCGGC
||  |   ||  |||  |  |||   |  |      |||  ||  ||  |          |
TCTCTGGCACCCTGACTAATAACCTTCAGGGCCACGCA..........C
                    .         .         .         .
ATTGACCGCCACCGCCCCCCAGGTCCGTAGGGACCAAAGAAGGGGCGGGA
  ||||||  |   |||  |||  ||||  ||   ||       |||   |        ||
TTTGACCACTCCCGACCCTCAGGCCCACAGATTAAAAAAGTGAACAATGA
                  . E-box   .         E-box     .         E-box .
GGAAGACTGTCACGTGGCGCCGGAGTTCACGTGACTCG...TACACATGA
|  ||  ||||||||  ||  |  |  |||||||||  |   ||||||||||
GCAA.ACTGTCACGTGATGCAGATGCTCACGTGACCAGAGCTACACATGA
                    .         .         .         .
CTTCCAGTCCCCGGGCGCCTCCTGGAGAGCAAGGACGCGGGGGAGCAGAG
||||||||||   |||||||||||||||||||||||||   ||  ||||||||
CTTCCAGTCCAAAGGCGCCTCCTGGAGAGCAAGGACGCAAGGAAGCAGAG
```

FIG. 4




```
human:  1   MAAASEPVDSGALWGLERPEPPPTRFHRVHGANIRVDPSGTRATRVESFAHGVCFSREPL 60
            MAA SE V  GA     RPEPPPTRFH+VHGANIR+DPSGTRATRVESFAHGVCFSREPL
mouse:  1   MAAPSEHVGLGAPRSPARPEPPPTRFHQVHGANIRMDPSGTRATRVESFAHGVCFSREPL 60

human:  61  APGQVFLVEIEEKELGWCGHLRLGLTALDPASLAPVPEFSLPDLVNLGHTWVFAITRHHN 120
            APGQVFLVEIEEKELGWCGHLRLGLTALDPASLA VPEFSLPDLV+LGH+WVFAITRHHN
mouse:  61  APGQVFLVEIEEKELGWCGHLRLGLTALDPASLAAVPEFSLPDLVSLGHSWVFAITRHHN 120

human:  121 RVPREGRPEAEAAAPSRPPTLLVEPYLRIEQFRIPRDRLVGRSRPGLYSHLLDQLYELNV 180
            RVPREG+PEAEAA PS P  LLVEPYLRIEQFRIPRDRLVGRSRPGLYSHLLDQLYE NV
mouse:  121 RVPREGQPEAEAAVPSGPQALLVEPYLRIEQFRIPRDRLVGRSRPGLYSHLLDQLYEQNV 180

human:  181 LPPTARRSRLGVLFCPRPDGTADMHIIINGEDMGPSARGLPAAQPLYAVVDVFASTKSVR 240
            LPPTARRSRLGVLFCPR DGTADMHIIINGEDMGPSARGLPAAQPLYAVVDVFASTKSVR
mouse:  181 LPPTARRSRLGVLFCPREDGTADMHIIINGEDMGPSARGLPAAQPLYAVVDVFASTKSVR 240

human:  241 LVQLEYGLPSLQTLCRLVIQRSMVHRLAIDGLHLPKELKDFCKYE 285
            LVQLEYGLPSLQTLCRLVIQ+ +VHRLAID LHLPK LKDFCKYE
mouse:  241 LVQLEYGLPSLQTLCRLVIQKRVVHRLAIDVLHLPKGLKDFCKYE 285
```

FIG. 5

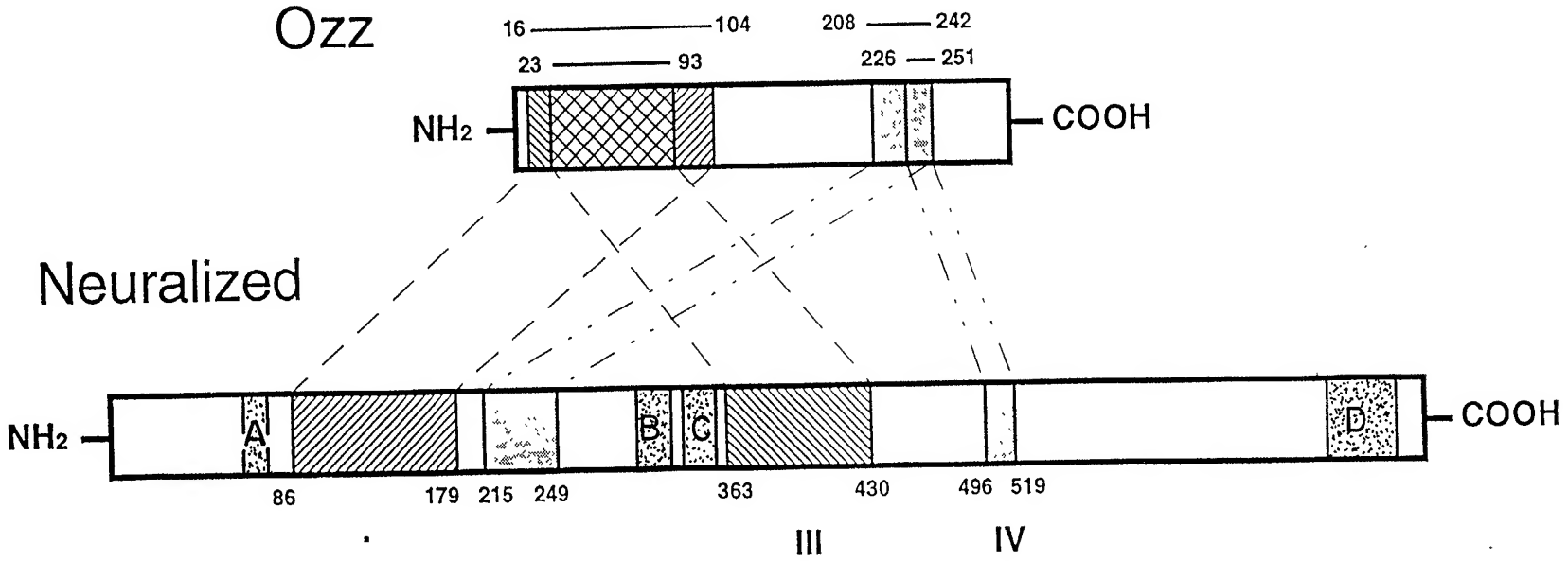


FIG. 6

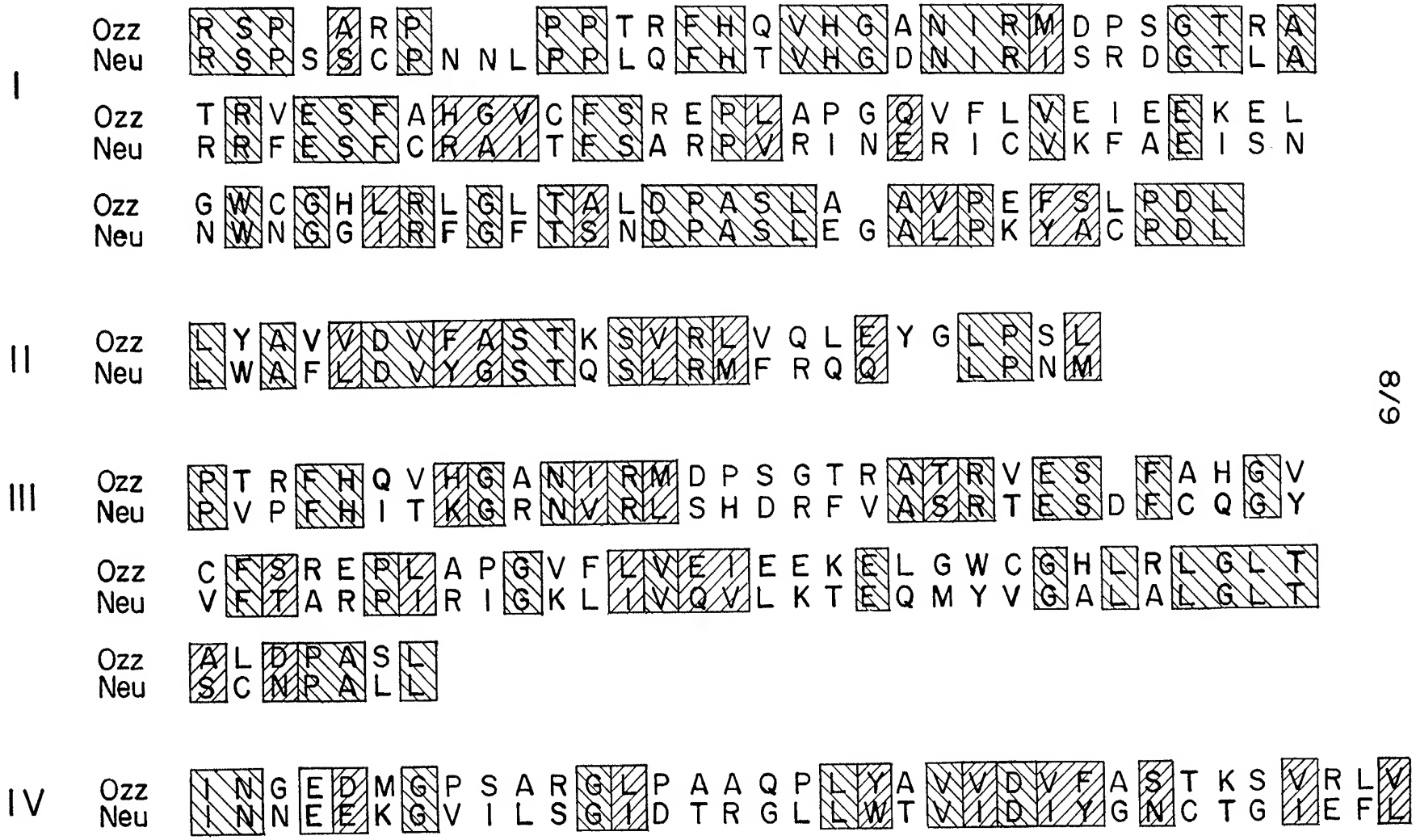
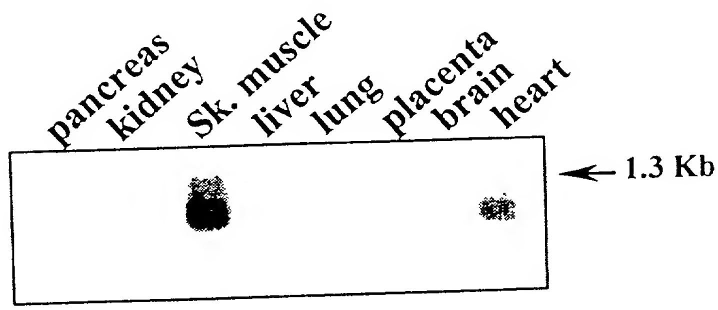


FIG. 7


pancreas
kidney
Sk. muscle
liver
lung
placenta
brain
heart
1.3 Kb

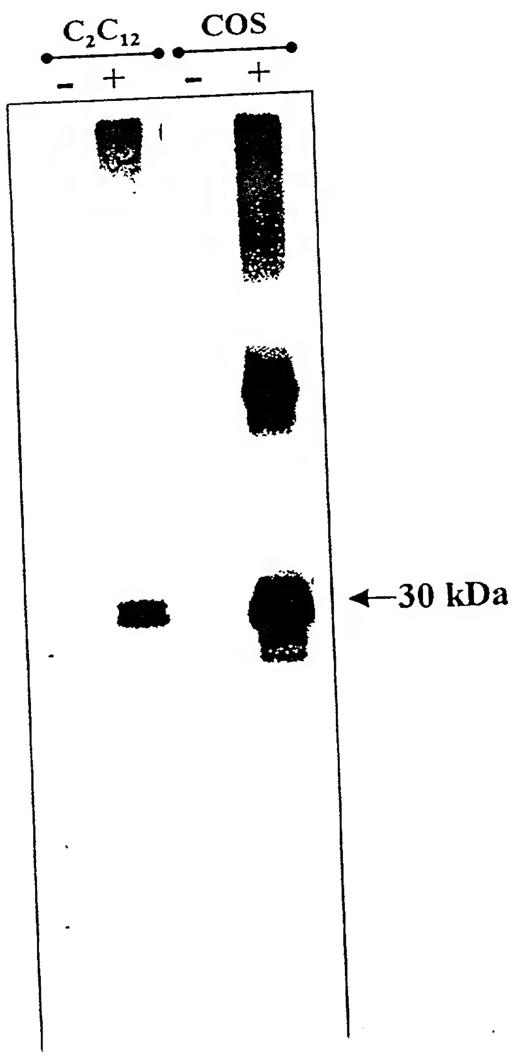

C_2C_{12}
COS
-
+
-
+
30 kDa

FIG. 8